

N. Minni Field

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/298,523B

DATE: 03/27/2001
 TIME: 10:47:51

Input Set : A:\Brilesal.app
 Output Set: N:\CRF3\03272001\I298523B.raw

RECEIVED

APR 06 2001

TECH CENTER 1600/2900

P#12

ENTERED

3 <110> APPLICANT: BRILES et al.
 5 <120> TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
 6 AND STRAINS THEREOF AND USES THEREFOR
 8 <130> FILE REFERENCE: 454312-3140
 10 <140> CURRENT APPLICATION NUMBER: 09/298,523B
 11 <141> CURRENT FILING DATE: 1999-04-23
 13 <160> NUMBER OF SEQ ID NOS: 78
 15 <170> SOFTWARE: PatentIn Ver. 2.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 691
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Streptococcus pneumoniae
 22 <400> SEQUENCE: 1
 23 Met Phe Ala Ser Lys Ser Glu Arg Lys Val His Tyr Ser Ile Arg Lys
 24 1 5 10 15
 26 Phe Ser Ile Gly Val Ala Ser Val Ala Val Ala Ser Leu Phe Leu Gly
 27 20 25 30
 29 Gly Val Val His Ala Glu Gly Val Arg Ser Gly Asn Asn Leu Thr Val
 30 35 40 45
 32 Thr Ser Ser Gly Gln Asp Ile Ser Lys Lys Tyr Ala Asp Glu Val Glu
 33 50 55 60
 35 Ser His Leu Glu Ser Ile Leu Lys Asp Val Lys Lys Asn Leu Lys Lys
 36 65 70 75 80
 38 Val Gln His Thr Gln Asn Val Gly Leu Ile Thr Lys Leu Ser Glu Ile
 39 85 90 95
 41 Lys Lys Lys Tyr Leu Tyr Asp Leu Lys Val Asn Val Leu Ser Glu Ala
 42 100 105 110
 44 Glu Leu Thr Ser Lys Thr Lys Glu Thr Lys Glu Lys Leu Thr Ala Thr
 45 115 120 125
 47 Phe Glu Gln Phe Lys Lys Asp Thr Leu Pro Thr Glu Pro Glu Lys Lys
 48 130 135 140
 50 Val Ala Glu Ala Gln Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu
 51 145 150 155 160
 53 Asp Gln Lys Glu Lys Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys
 54 165 170 175
 56 Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala
 57 180 185 190
 59 Glu Leu Glu Leu Val Lys Val Lys Ala Lys Glu Ser Gln Asp Glu Glu
 60 195 200 205
 62 Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln Ala Glu Ala
 63 210 215 220
 65 Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala Lys Arg Lys
 66 225 230 235 240
 68 Ala Asp Ala Lys Leu Lys Glu Ala Val Glu Lys Asn Val Ala Thr Ser
 69 245 250 255
 71 Glu Gln Asp Lys Pro Lys Arg Arg Ala Lys Arg Gly Val Ser Gly Glu
 72 260 265 270

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74 Leu Ala Thr Pro Asp Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser
75      275      280      285
77 Ser Val Gly Glu Glu Thr Leu Pro Ser Pro Ser Leu Asn Met Ala Asn
78      290      295      300
80 Glu Ser Gln Thr Glu His Arg Lys Asp Val Asp Glu Tyr Ile Lys Lys
81 305      310      315      320
83 Met Leu Ser Glu Ile Gln Leu Asp Arg Arg Lys His Thr Gln Asn Val
84      325      330      335
86 Asn Leu Asn Ile Lys Leu Ser Ala Ile Lys Thr Lys Tyr Leu Tyr Glu
87      340      345      350
89 Leu Ser Val Leu Lys Glu Asn Ser Lys Lys Glu Glu Leu Thr Ser Lys
90      355      360      365
92 Thr Lys Ala Glu Leu Thr Ala Ala Phe Glu Gln Phe Lys Lys Asp Thr
93      370      375      380
95 Leu Lys Pro Glu Lys Lys Val Ala Glu Ala Glu Lys Lys Val Glu Glu
96 385      390      395      400
98 Ala Lys Lys Lys Ala Lys Asp Gln Lys Glu Glu Asp Arg Arg Asn Tyr
99      405      410      415
101 Pro Thr Asn Thr Tyr Lys Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp
102      420      425      430
104 Val Lys Val Lys Glu Ala Glu Leu Glu Leu Val Lys Glu Glu Ala Asn
105      435      440      445
107 Glu Ser Arg Asn Glu Glu Lys Ile Lys Gln Ala Lys Glu Lys Val Glu
108      450      455      460
110 Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu Lys Ile Lys Thr Asp Arg
111 465      470      475      480
113 Lys Lys Ala Glu Glu Glu Ala Lys Arg Lys Ala Glu Glu Ser Glu Lys
114      485      490      495
116 Lys Ala Ala Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Tyr Ala Leu
117      500      505      510
119 Glu Ala Lys Ile Ala Glu Leu Glu Tyr Glu Val Gln Arg Leu Glu Lys
120      515      520      525
122 Glu Leu Lys Glu Ile Asp Glu Ser Asp Ser Glu Asp Tyr Leu Lys Glu
123      530      535      540
125 Gly Leu Arg Ala Pro Leu Gln Ser Lys Leu Asp Thr Lys Lys Ala Lys
126 545      550      555      560
128 Leu Ser Lys Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala
129      565      570      575
131 Glu Ile Ala Lys Leu Glu Val Gln Leu Lys Asp Ala Glu Gly Asn Asn
132      580      585      590
134 Asn Val Glu Ala Tyr Phe Lys Glu Gly Leu Glu Lys Thr Thr Ala Glu
135      595      600      605
137 Lys Lys Ala Glu Leu Glu Lys Ala Glu Ala Asp Leu Lys Lys Ala Val
138      610      615      620
140 Asp Glu Pro Glu Thr Pro Ala Pro Ala Pro Gln Pro Ala Pro Ala Pro
141 625      630      635      640
143 Glu Lys Pro Ala Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro
144      645      650      655
146 Ala Pro Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Pro

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147          660          665          670
149 Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Thr Pro Glu Thr
150          675          680          685
152 Pro Lys Thr
153          690
156 <210> SEQ ID NO: 2
157 <211> LENGTH: 707
158 <212> TYPE: PRT
159 <213> ORGANISM: Streptococcus pneumoniae
161 <400> SEQUENCE: 2
162 Met Phe Ala Ser Lys Ser Glu Arg Lys Val His Tyr Ser Ile Arg Lys
163 1 5 10 15
165 Phe Ser Ile Gly Val Ala Ser Val Ala Val Ala Ser Leu Phe Leu Gly
166 20 25 30
168 Gly Val Val His Ala Glu Gly Val Arg Ser Gly Asn Asn Leu Thr Val
169 35 40 45
171 Thr Ser Ser Gly Gln Asp Ile Ser Lys Lys Tyr Ala Asp Glu Val Glu
172 50 55 60
174 Ser His Leu Glu Ser Ile Leu Lys Asp Val Lys Lys Asn Leu Lys Lys
175 65 70 75 80
177 Val Gln His Thr Gln Asn Val Gly Leu Ile Thr Lys Leu Ser Glu Ile
178 85 90 95
180 Lys Lys Lys Tyr Leu Tyr Asp Leu Lys Val Asn Val Leu Ser Glu Ala
181 100 105 110
183 Glu Leu Thr Ser Lys Thr Lys Glu Thr Lys Glu Lys Leu Thr Ala Thr
184 115 120 125
186 Phe Glu Gln Phe Lys Lys Asp Thr Leu Pro Thr Glu Pro Glu Lys Lys
187 130 135 140
189 Val Ala Glu Ala Gln Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu
190 145 150 155 160
192 Asp Gln Lys Glu Lys Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys
193 165 170 175
195 Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala
196 180 185 190
198 Glu Leu Glu Leu Val Lys Val Lys Ala Lys Glu Ser Gln Asp Glu Glu
199 195 200 205
201 Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln Ala Glu Ala
202 210 215 220
204 Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala Lys Arg Lys
205 225 230 235 240
207 Ala Asp Ala Lys Leu Lys Glu Ala Val Glu Lys Asn Val Ala Thr Ser
208 245 250 255
210 Glu Gln Asp Lys Pro Lys Arg Arg Ala Lys Arg Gly Val Ser Gly Glu
211 260 265 270
213 Leu Ala Thr Pro Asp Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser
214 275 280 285
216 Ser Val Gly Glu Glu Thr Leu Pro Ser Pro Ser Leu Asn Met Ala Asn
217 290 295 300
219 Glu Ser Gln Thr Glu His Arg Lys Asp Val Asp Glu Tyr Ile Lys Lys

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220 305          310          315          320
222 Met Leu Ser Glu Ile Gln Leu Asp Gly Arg Lys His Thr Pro Asn Val
223          325          330          335
225 Asn Leu Asn Ile Lys Leu Ser Ala Ile Lys Thr Lys Tyr Leu Tyr Glu
226          340          345          350
228 Leu Ser Val Leu Lys Glu Asn Ser Lys Lys Glu Glu Leu Thr Ser Lys
229          355          360          365
231 Thr Lys Lys Ala Glu Leu Thr Ala Ala Phe Glu Gln Phe Lys Lys Asp Thr
232          370          375          380
234 Leu Lys Pro Glu Lys Lys Val Ala Glu Ala Glu Lys Lys Val Glu Glu
235 385          390          395          400
237 Ala Lys Lys Lys Ala Lys Asp Gln Lys Glu Glu Asp Arg Arg Asn Tyr
238          405          410          415
240 Pro Thr Asn Thr Tyr Lys Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp
241          420          425          430
243 Val Lys Val Lys Glu Ala Glu Leu Glu Leu Val Lys Glu Glu Ala Asn
244          435          440          445
246 Glu Ser Arg Asn Glu Glu Lys Ile Lys Gln Ala Lys Glu Lys Val Glu
247          450          455          460
249 Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu Lys Ile Lys Thr Asp Arg
250 465          470          475          480
252 Lys Lys Ala Glu Glu Glu Ala Lys Arg Lys Ala Glu Glu Ser Glu Lys
253          485          490          495
255 Lys Ala Ala Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Tyr Ala Leu
256          500          505          510
258 Glu Ala Lys Ile Ala Glu Leu Glu Tyr Glu Val Gln Arg Leu Glu Lys
259          515          520          525
261 Glu Leu Lys Glu Ile Asp Glu Ser Asp Ser Glu Asp Tyr Leu Lys Glu
262          530          535          540
264 Gly Leu Arg Ala Pro Leu Gln Ser Lys Leu Asp Thr Lys Lys Ala Lys
265 545          550          555          560
267 Leu Ser Lys Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala
268          565          570          575
270 Glu Ile Ala Lys Leu Glu Val Gln Leu Lys Asp Ala Glu Gly Asn Asn
271          580          585          590
273 Asn Val Glu Ala Tyr Phe Lys Glu Gly Leu Glu Lys Thr Thr Ala Glu
274          595          600          605
276 Lys Lys Ala Glu Leu Glu Lys Ala Glu Ala Asp Leu Lys Lys Ala Val
277          610          615          620
279 Asp Glu Pro Glu Thr Pro Ala Pro Ala Pro Gln Pro Ala Pro Ala Pro
280 625          630          635          640
282 Glu Lys Pro Ala Glu Lys Pro Ala Pro Ala Pro Ala Pro Glu Lys Pro
283          645          650          655
285 Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro
286          660          665          670
288 Ala Pro Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Pro
289          675          680          685
291 Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Thr Pro Lys
292          690          695          700

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294 Pro Glu Thr
295 705
298 <210> SEQ ID NO: 3
299 <211> LENGTH: 711
300 <212> TYPE: PRT
301 <213> ORGANISM: Streptococcus pneumoniae
303 <400> SEQUENCE: 3
304 Met Phe Ala Ser Lys Ser Glu Arg Lys Val His Tyr Ser Ile Arg Lys
305 1 5 10 15
307 Phe Ser Ile Gly Val Ala Ser Val Val Ala Ser Leu Val Met Gly
308 20 25 30
310 Ser Val Val His Ala Thr Glu Asn Glu Gly Ile Thr Gln Val Ala Thr
311 35 40 45
313 Ser Tyr Asn Lys Ala Asn Glu Ser Gln Thr Glu His Arg Lys Ala Ala
314 50 55 60
316 Lys Gln Val Asp Glu Asp Ile Lys Lys Met Leu Ser Glu Ile Gln Glu
317 65 70 75 80
319 Tyr Ile Lys Lys Met Leu Ser Glu Ile Gln Leu Asp Lys Arg Lys His
320 85 90 95
322 Thr Gln Asn Val Asn Leu Asn Arg Lys Leu Ser Ala Ile Gln Thr Lys
323 100 105 110
325 Tyr Leu Tyr Glu Leu Arg Val Leu Lys Glu Lys Ser Lys Lys Glu Glu
326 115 120 125
328 Leu Thr Ser Lys Thr Lys Lys Glu Leu Asp Ala Ala Phe Glu Lys Phe
329 130 135 140
331 Lys Lys Glu Glu Pro Glu Leu Thr Lys Lys Leu Ala Glu Ala Lys Gln
332 145 150 155 160
334 Lys Ala Lys Ala Gln Lys Glu Glu Asp Phe Arg Asn Tyr Pro Thr Asn
335 165 170 175
337 Thr Tyr Lys Thr Leu Glu Leu Glu Ile Ala Glu Phe Asp Val Lys Val
338 180 185 190
340 Lys Glu Ala Glu Leu Glu Leu Val Lys Glu Glu Ala Lys Pro Arg Asn
341 195 200 205
343 Glu Glu Lys Ile Lys Gln Ala Lys Ala Lys Val Glu Ser Lys Lys Ala
344 210 215 220
346 Glu Ala Thr Arg Leu Glu Glu Ile Lys Thr Glu Arg Lys Lys Ala Glu
347 225 230 235 240
349 Glu Glu Ala Lys Arg Lys Ala Glu Glu Ser Glu Lys Lys Ala Ala Glu
350 245 250 255
352 Ala Lys Gln Lys Val Asp Thr Lys Glu Gln Gly Lys Pro Lys Arg Arg
353 260 265 270
355 Ala Lys Arg Gly Val Ser Gly Glu Leu Ala Thr Pro Asp Lys Lys Glu
356 275 280 285
358 Asn Asp Ala Lys Ser Ser Asp Ser Ser Val Gly Glu Glu Thr Leu Pro
359 290 295 300
361 Ser Pro Ser Leu Asn Ala Met Ala Asn Glu Ser Gln Thr Glu His Arg
362 305 310 315 320
364 Lys Asp Val Asp Glu Tyr Ile Lys Lys Met Leu Ser Glu Ile Gln Leu
365 325 330 335

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 03/27/2001
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Input Set : A:\Brilesal.app
Output Set: N:\CRF3\03272001\I298523B.raw

L:1669 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:4354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:4492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74